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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/941,936A

DATE: 02/26/2002

TIME: 13:54:23

Input Set : A:\032301.202.seq.ST25.txt

Output Set: N:\CRF3\02262002\I941936A.raw

3 <110> APPLICANT: BATHE, Brigitte, et al.
 5 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE sigD GENE
 7 <130> FILE REFERENCE: 032301 WD 202
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/941,936A
 C--> 9 <141> CURRENT FILING DATE: 2001-08-30
 9 <160> NUMBER OF SEQ ID NOS: 4
 11 <170> SOFTWARE: PatentIn version 3.1
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 1109
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Corynebacterium glutamicum
 18 <220> FEATURE:
 19 <221> NAME/KEY: CDS
 20 <222> LOCATION: (300)..(878)
 21 <223> OTHER INFORMATION:
 24 <400> SEQUENCE: 1

| | | | |
|----|---|-------------------------|-----|
| 25 | tggaaactgg tgccttgtt ggcgggttgt gtttccagaa agctttggac | gcattccgc | 60 |
| 27 | atctacgatc tggctctgctg ctgacttctc agacatttagc | attcccttc | 120 |
| 29 | ttacctatgg attaagtctg attgatagtc tacatcagaa | tgtcacttcg | 180 |
| 31 | taatcagccc ttacgtaaac tgccagaaaa aagacaaaaag | cgccaccaaa | 240 |
| 33 | ttgacaccccttacacacactt atatggtaccccgtctga | actggtattc | 299 |
| 35 | gtg aag tca aaa gag cgt aac gac gcc cac gtc acc | tgagcaatt | 347 |
| 36 | Met Lys Ser Lys Glu Arg Asn Asp Ala His Val Thr | Glu Leu Ala Leu | |
| 37 | 1 5 10 15 | | |
| 39 | gcc gcc ggc cgt ggc gac cgc gca gct ctc acc | gat ttc atc | 395 |
| 40 | Ala Ala Gly Arg Gly Asp Arg Ala Ala Leu Thr | Asp Phe Ile Arg Glu | |
| 41 | 20 25 30 | | |
| 43 | acc caa gac gat gtc tgg cgt ctc ctc gcc cac | ctt ggc ggc cac gaa | 443 |
| 44 | Thr Gln Asp Asp Val Trp Arg Leu Leu Ala His | Leu Gly His Glu | |
| 45 | 35 40 45 | | |
| 47 | atc gcc gac gat cta acc caa gaa act tat ctg | cggt gtc atg agc | 491 |
| 48 | Ile Ala Asp Asp Leu Thr Gln Glu Thr Tyr Leu | Arg Val Met Ser Ala | |
| 49 | 50 55 60 | | |
| 51 | ctc ccc cgc ttc gca gcg cgc tcc tcg | gct acc tgg cta cta tcg | 539 |
| 52 | Leu Pro Arg Phe Ala Ala Arg Ser Ser Ala Arg | Thr Trp Leu Leu Ser | |
| 53 | 65 70 75 80 | | |
| 55 | cta gcc cgg cgc gtc tgg gtc gac aac atc | cga cac gac atg gca | 587 |
| 56 | Leu Ala Arg Arg Val Trp Val Asp Asn Ile Arg | His Asp Met Ala Arg | |
| 57 | 85 90 95 | | |
| 59 | ccc cgc aaa tcc atc gtc gaa tac gaa | gac acc ggt gcc acc gac | 635 |
| 60 | Pro Arg Lys Ser Ile Val Glu Tyr Glu Asp Thr | Gly Ala Thr Asp Ala | |
| 61 | 100 105 110 | | |
| 63 | agc aac gca ggc atc tgg tcc gag tgg atc | gac gtg cgc acg ctt atc | 683 |

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|-----|------------|------------|----------------------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|
| 64 | Ser | Asn | Ala | Gly | Ile | Trp | Ser | Glu | Trp | Ile | Asp | Val | Arg | Thr | Leu | Ile | |
| 65 | 115 | | | | | 120 | | | | | | | | | 125 | | |
| 67 | gac | gcc | ctc | cca | ccc | gaa | cgc | cgc | gaa | gcc | ctc | atc | ctc | acc | caa | gtg | 731 |
| 68 | Asp | Ala | Leu | Pro | Pro | Glu | Arg | Arg | Glu | Ala | Leu | Ile | Leu | Thr | Gln | Val | |
| 69 | 130 | | | | | 135 | | | | | | | | | 140 | | |
| 71 | ttg | ggc | tac | acc | tac | gaa | gaa | gcc | gca | aaa | atc | gcc | gac | gtc | cga | gtc | 779 |
| 72 | Leu | Gly | Tyr | Thr | Tyr | Glu | Glu | Ala | Ala | Lys | Ile | Ala | Asp | Val | Arg | Val | |
| 73 | 145 | | | | | 150 | | | | | | | | | 155 | 160 | |
| 75 | gga | aca | atc | cgt | tcc | cgc | gta | gcc | cgc | aga | gac | ctc | att | gct | | 827 | |
| 76 | Gly | Thr | Ile | Arg | Ser | Arg | Val | Ala | Arg | Ala | Arg | Ala | Asp | Leu | Ile | Ala | |
| 77 | 165 | | | | | 170 | | | | | | | | | 175 | | |
| 79 | gca | aca | gct | acc | ggt | gat | tcc | tca | gcc | gaa | gat | ggc | aaa | tcc | gcc | caa | 875 |
| 80 | Ala | Thr | Ala | Thr | Gly | Asp | Ser | Ser | Ala | Glu | Asp | Gly | Lys | Ser | Ala | Gln | |
| 81 | 180 | | | | | 185 | | | | | | | | | 190 | | |
| 83 | ggt | tagcagatga | gctacgtcaa | cggcgtaatc | ccttaaccag | attgctaatt | | | | | | | | | | 928 | |
| 84 | Gly | | | | | | | | | | | | | | | | |
| 87 | tacagttcta | ttttgtgtct | cgatcaaagc | gactcttacc | caccctagaa | tcctttgacc | | | | | | | | | | 988 | |
| 89 | gcatcaacac | tttgtttta | tctaaaactg | aatctttaat | ttttacgctc | gcagatgatt | | | | | | | | | | 1048 | |
| 91 | ttcctccagc | aatggaagta | ataaccccgc | cccgaacgac | agctttcga | ggtgcgcttc | | | | | | | | | | 1108 | |
| 93 | c | | | | | | | | | | | | | | | 1109 | |
| 96 | <210> | SEQ ID NO: | 2 | | | | | | | | | | | | | | |
| 97 | <211> | LENGTH: | 193 | | | | | | | | | | | | | | |
| 98 | <212> | TYPE: | PRT | | | | | | | | | | | | | | |
| 99 | <213> | ORGANISM: | Corynebacterium glutamicum | | | | | | | | | | | | | | |
| 101 | <400> | SEQUENCE: | 2 | | | | | | | | | | | | | | |
| 103 | Met | Lys | Ser | Lys | Glu | Arg | Asn | Asp | Ala | His | Val | Thr | Glu | Leu | Ala | Leu | |
| 104 | 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| 107 | Ala | Ala | Gly | Arg | Gly | Asp | Arg | Ala | Ala | Leu | Thr | Asp | Phe | Ile | Arg | Glu | |
| 108 | | | | | 20 | | | | | 25 | | | | | 30 | | |
| 111 | Thr | Gln | Asp | Asp | Val | Trp | Arg | Leu | Leu | Ala | His | Leu | Gly | Gly | His | Glu | |
| 112 | | | | | 35 | | | | | 40 | | | | | 45 | | |
| 115 | Ile | Ala | Asp | Asp | Leu | Thr | Gln | Glu | Thr | Tyr | Leu | Arg | Val | Met | Ser | Ala | |
| 116 | | | | | 50 | | | | | 55 | | | | | 60 | | |
| 119 | Leu | Pro | Arg | Phe | Ala | Ala | Arg | Ser | Ser | Ala | Arg | Thr | Trp | Leu | Ser | | |
| 120 | 65 | | | | 70 | | | | | 75 | | | | | 80 | | |
| 123 | Leu | Ala | Arg | Arg | Val | Trp | Val | Asp | Asn | Ile | Arg | His | Asp | Met | Ala | Arg | |
| 124 | | | | | 85 | | | | | 90 | | | | | 95 | | |
| 127 | Pro | Arg | Lys | Ser | Ile | Val | Glu | Tyr | Glu | Asp | Thr | Gly | Ala | Thr | Asp | Ala | |
| 128 | | | | | 100 | | | | | 105 | | | | | 110 | | |
| 131 | Ser | Asn | Ala | Gly | Ile | Trp | Ser | Glu | Trp | Ile | Asp | Val | Arg | Thr | Leu | Ile | |
| 132 | | | | | 115 | | | | | 120 | | | | | 125 | | |
| 135 | Asp | Ala | Leu | Pro | Pro | Glu | Arg | Arg | Glu | Ala | Leu | Ile | Leu | Thr | Gln | Val | |
| 136 | | | | | 130 | | | | | 135 | | | | | 140 | | |
| 139 | Leu | Gly | Tyr | Thr | Tyr | Glu | Glu | Ala | Ala | Lys | Ile | Ala | Asp | Val | Arg | Val | |
| 140 | 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| 143 | Gly | Thr | Ile | Arg | Ser | Arg | Val | Ala | Arg | Ala | Arg | Ala | Asp | Leu | Ile | Ala | |
| 144 | | | | | | 165 | | | | | 170 | | | | | 175 | |
| 147 | Ala | Thr | Ala | Thr | Gly | Asp | Ser | Ser | Ala | Glu | Asp | Gly | Lys | Ser | Ala | Gln | |
| 148 | | | | | | 180 | | | | | 185 | | | | | 190 | |

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151 Gly
155 <210> SEQ ID NO: 3
156 <211> LENGTH: 28
157 <212> TYPE: DNA
158 <213> ORGANISM: Corynebacterium glutamicum
160 <400> SEQUENCE: 3
161 acggtaaaaa ctacacacct ttatggtg 28
164 <210> SEQ ID NO: 4
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166 <212> TYPE: DNA
167 <213> ORGANISM: Corynebacterium glutamicum
169 <400> SEQUENCE: 4
170 gctctagagt tgacgttagct catctgct 28

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/941,936A

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Input Set : A:\032301.202.seq.ST25.txt

Output Set: N:\CRF3\02262002\I941936A.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date